

*Minifed*

## RAW SEQUENCE LISTING ERROR REPORT



*#7*

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/004,395

Art Unit / Team No.: 1643

Date Processed by STIC: 1/15/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/004,395DATE: 01/15/1999  
TIME: 12:46:41

Input Set: I004395.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

1 <110> Gilmore Jr., Robert D  
 2 Johnson, Barbara JB  
 3 <120> RECOMBINANT P37/FlaA AS A DIAGNOSTIC REAGENT  
 4 <130> 97,429  
 5 <140> US/09/004,395  
 6 <141> 1998-01-08  
 W--> 7 ~~<150>~~ delete these numbers identified if you don't have responses for them  
 E--> 8 <151>  
 9 <160> ~~⑥~~ 7 shown in file - do not put a & before the <160> response  
 10 <170> Microsoft Word 97

Does Not Comply  
Corrected Diskette Note J

## ERRORED SEQUENCES FOLLOW

Attention Consult new  
Sequence Rule

E--> 11 <210> 1  
 12 <211> ~~1655~~ 1832 ntors (p 3)  
 13 <212> DNA  
 E--> 14 <213> ↑ move up - <220> does not have a response (it is a header only)  
 15 <220> Unknown → (see item 12 in Error summary first)  
 16 <221> CDS  
 17 <222> 473..1498 → error (220)  
 18 <221> sig\_peptide  
 19 <222> 473..538 → error (220)  
 20 <221> mat\_peptide  
 21 <222> 539..1498  
 22 <223>  
 23 <400> 1  
 24 atgataatct ttttcaaaa aaggttttt atttcattc tagcaaggga tttgttgcta 60  
 25 atttaagata tttaagagat gaacaaaatt tggaaagataa ttttagatctt ttagtaaaag 120  
 26 attttctttt aggaagcaat gaggggtttt ctttgggtt ttttattaatg gattcaagat 180  
 27 ttttatattc tttttaaag aatggatgtt attatgtaaa tctttcaaga gaattttatg 240  
 28 attctttaa taatggatgt tataatgaat ctttgtatgt taaggtcaat cttttgcta 300  
 29 tgtcttaat aaaaacaatg cgctttaact atcctggtaa gataaaaaag attattttc 360

14 Lys Arg Lys Ala Lys Ser Ile Leu Phe Phe Leu Leu Ser Thr Val Leu  
 15 -20 -15 -10  
 36

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cct gga gaa tta gtc tta gat ttt gcc gag ctt gca aga gat cca agt	619
Pro Gly Leu Val Leu Asp Phe Ala Glu Leu Ala Arg Asp Pro Ser	
15 20 25	
tca act aga ctt gat ctt aca aat tat gtt gat tat gta tat tcg ggc	667
Ser Thr Arg Leu Asp Leu Thr Asn Tyr Val Asp Tyr Val Tyr Ser Gly	
30 35 40	
gct tct ggt att gtt aag ccg gaa gat atg gtt gta gat ctt ggg ata	715
Ala Ser Gly Ile Val Lys Pro Glu Asp Met Val Val Asp Leu Gly Ile	
45 50 55	
aat aat tgg agc gtt tta ctt act cct tct gca agg ttg cag gct tac	763
Asn Asn Trp Ser Val Leu Leu Thr Pro Ser Ala Arg Leu Gln Ala Tyr	
60 65 70 75	
gtt aaa aat tca gtt gtt gcg ccc gct gtt gtt aag agt gag tca aaa	811
Val Lys Asn Ser Val Val Ala Pro Ala Val Val Lys Ser Glu Ser Lys	
80 85 90	
agg tac gca ggt gat act att ttg ggg gta aga gtt ttg ttt cca agc	859
Arg Tyr Ala Gly Asp Thr Ile Leu Gly Val Arg Val Leu Phe Pro Ser	
95 100 105	
tat tct caa tca tct gct atg att atg cca cca ttt aaa att cct ttt	907
Tyr Ser Gln Ser Ser Ala Met Ile Met Pro Pro Phe Lys Ile Pro Phe	
110 115 120	
tat tca ggg gaa agt ggc aat caa ttt tta ggc aaa ggt ctt att gat	955
Tyr Ser Gly Glu Ser Gly Asn Gln Phe Leu Gly Lys Gly Leu Ile Asp	
125 130 135	
aac att aaa acc atg aaa gaa att aag gta tct gtt tat agt tta ggg	1003
Asn Ile Lys Thr Met Lys Glu Ile Lys Val Ser Val Tyr Ser Leu Gly	
140 145 150 155	
tat gag ata gat ctt gag gtt tta ttt gaa gat atg aat ggc atg gaa	1051
Tyr Glu Ile Asp Leu Glu Val Leu Phe Glu Asp Met Asn Gly Met Glu	
160 165 170	
tat gct tat tct atg ggt act tta aag ttt aaa ggg tgg gct gat tta	1099
Tyr Ala Tyr Ser Met Gly Thr Leu Lys Phe Lys Gly Trp Ala Asp Leu	
175 180 185	
att tgg tca aat cct aac tat att cct aat ata tca tcc aga att att	1147
Ile Trp Ser Asn Pro Asn Tyr Ile Pro Asn Ile Ser Ser Arg Ile Ile	
190 195 200	
lys Ala Phe Arg Val Ser Lys Ser His Ser Ser Lys Val Lys Asn Phe	
220 225 230 235	

89/CC4 345

Ile Phe Tyr Val Lys Asp Leu Arg Val Leu Tyr Asp Lys Leu Ser Val  
240 245 250

tca ata gat tct gat att gac agt gag tct gta ttt aaa gtt tat gag 1339  
Ser Ile Asp Ser Asp Ile Asp Ser Glu Ser Val Phe Lys Val Tyr Glu  
255 260 265

act agc gga act gaa tcc ctt cgt aaa tta aag gca cac gaa act ttt 1387  
Thr Ser Gly Thr Glu Ser Leu Arg Lys Leu Lys Ala His Glu Thr Phe  
270 275 280

aaa aga gtt tta aag ctt aga gaa aaa att tct atc gct gaa ggc tct 1435  
Lys Arg Val Leu Lys Leu Arg Glu Lys Ile Ser Ile Ala Glu Gly Ser  
285 290 295

ttc caa aac ttt gta gaa aag att gag agt gaa aaa cct gaa gaa tca 1483  
Phe Gln Asn Phe Val Glu Lys Ile Glu Ser Glu Lys Pro Glu Glu Ser  
300 305 310 315

tct ccg aaa aat tag gtttaaatta atatgtaaag ctacctaaaa ggtttgcttt 1538  
Ser Pro Lys Asn \*  
320

acatattaaa ataataggaa atagtatatg gaaatattag atttgaaaaa tgaagagctt 1598

ttaggagttt ttttgaaga agctcaaaat cttgtagata tccttgaaga gaatatt 1655

gcggccgcaa tgtgagttt ttagtttga tttgctcccc cggcgtcggtt caatgagaat 60/1715  
ggataagagg ctcgtggat tgacgtgagg gggcagggat ggctataatt ctgggagcga 120/1775  
actccggcga aatatgaagc gcatcgatac aagtgagttg tagggaggga accatgg 177/1832

<210> 2 755 (new in next start)

<211> 342

<212> PRT → DNA

<213> Unknown → see item 12

<220>

<221>

<222>

<223>

<400> 2

ttgacgtgag gggcagggta tggcttatatt tctggagcg aactccggc gaata

55

<210> 3 341 (new in next start)

<211> 55

<212> DNA PRT

<213> Mung bean

Leu Phe Ala Gln Glu Thr Asp Gly Leu Ala Glu Gly Ser Lys Arg Ala

07/02/74, 345

Glu Pro Gly Glu Leu Val Leu Asp Phe Ala Glu Leu Ala Arg Asp Pro  
15 20 25

Ser Ser Thr Arg Leu Asp Leu Thr Asn Tyr Val Asp Tyr Val Tyr Ser  
30 35 40

Gly Ala Ser Gly Ile Val Lys Pro Glu Asp Met Val Val Asp Leu Gly  
45 50 55

Ile Asn Asn Trp Ser Val Leu Leu Thr Pro Ser Ala Arg Leu Gln Ala  
60 65 70

Tyr Val Lys Asn Ser Val Val Ala Pro Ala Val Val Lys Ser Glu Ser  
75 80 85 90

Lys Arg Tyr Ala Gly Asp Thr Ile Leu Gly Val Arg Val Leu Phe Pro  
95 100 105

Ser Tyr Ser Gln Ser Ser Ala Met Ile Met Pro Pro Phe Lys Ile Pro  
110 115 120

Phe Tyr Ser Gly Glu Ser Gly Asn Gln Phe Leu Gly Lys Gly Leu Ile  
125 130 135

Asp Asn Ile Lys Thr Met Lys Glu Ile Lys Val Ser Val Tyr Ser Leu  
140 145 150

Gly Tyr Glu Ile Asp Leu Glu Val Leu Phe Glu Asp Met Asn Gly Met  
155 160 165 170

Glu Tyr Ala Tyr Ser Met Gly Thr Leu Lys Phe Lys Gly Trp Ala Asp  
175 180 185

Leu Ile Trp Ser Asn Pro Asn Tyr Ile Pro Asn Ile Ser Ser Arg Ile  
190 195 200

Ile Lys Asp Asp Val Pro Asn Tyr Pro Leu Ala Ser Ser Lys Met Arg  
205 210 215

Phe Lys Ala Phe Arg Val Ser Lys Ser His Ser Ser Lys Val Lys Asn  
220 225 230

Phe Ile Phe Tyr Val Lys Asp Leu Arg Val Leu Tyr Asp Lys Leu Ser  
235 240 245 250

Val Ser Ile Asp Ser Asp Ile Asp Ser Glu Ser Val Phe Lys Val Tyr  
255 260 265

Ser Phe Gln Asn Phe Val Glu Tyr Ile Ile Ser Glu Lys Pro Ile Ile

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Ser Ser Pro Lys Asn  
315 ~~20~~ <sup>\*</sup> delete

<210> 3  
<211> 21  
<212> DNA  
<213> Unknown <sup>rem 12</sup>  
<400> 3  
atgaaaagga aagctaaaag t

21

<210> 4  
<211> 19  
<212> DNA  
<213> Unknown <sup>rem 12</sup>  
<400> 4  
gatggatttag cagagggtt

19

<210> 5  
<211> 21  
<212> DNA  
<213> Unknown <sup>rem 12</sup>  
<400> 5  
tgggataaat aattggagcg t

21

<210> 6  
<211> 21  
<212> DNA  
<213> Unknown <sup>rem 12</sup>  
<400> 6  
ctaatttttc ggagatgatt c

21

(1) 604